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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Schlessinger, Joseph
Sap, Jan M.
- (ii) TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
PHOSPHATASE-ALPHA
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS
 - (B) STREET: 1155 AVENUE OF THE AMERICAS
 - (C) CITY: NEW YORK
 - (D) STATE: NEW YORK
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/015,985
 - (B) FILING DATE: 10-FEB-1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7683-020
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
 - (B) TELEFAX: (212) 869-9741/8864
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 802 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Asp Ser Trp Phe Ile Leu Val Leu Leu Gly Ser Gly Leu Ile Cys
 1           5           10           15
Val Ser Ala Asn Asn Ala Thr Thr Val Ala Pro Ser Val Gly Ile Thr
          20           25           30
Arg Leu Ile Asn Ser Ser Thr Ala Glu Pro Val Lys Glu Glu Ala Lys
          35           40           45
Thr Ser Asn Pro Thr Ser Ser Leu Thr Ser Leu Ser Val Ala Pro Thr
          50           55           60
```

Phe Ser Pro Asn Ile Thr Leu Gly Pro Thr Tyr Leu Thr Thr Val Asn
 65 70 75 80
 Ser Ser Asp Ser Asp Asn Gly Thr Thr Arg Thr Ala Ser Thr Asn Ser
 85 90 95
 Ile Gly Ile Thr Ile Ser Pro Asn Gly Thr Trp Leu Pro Asp Asn Gln
 100 105 110
 Phe Thr Asp Ala Arg Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
 115 120 125
 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ser Gly Asn Ser Asp Ser Lys
 130 135 140
 Asp Arg Arg Asp Glu Thr Pro Ile Ile Ala Val Met Val Ala Leu Ser
 145 150 155 160
 Ser Leu Leu Val Ile Val Phe Ile Ile Ile Val Leu Tyr Met Leu Arg
 165 170 175
 Phe Lys Lys Tyr Lys Gln Ala Gly Ser His Ser Asn Ser Phe Arg Leu
 180 185 190
 Ser Asn Gly Arg Thr Glu Asp Val Glu Pro Gln Ser Val Pro Leu Leu
 195 200 205
 Ala Arg Ser Pro Ser Thr Asn Arg Lys Tyr Pro Pro Leu Pro Val Asp
 210 215 220
 Lys Leu Glu Glu Glu Ile Asn Arg Arg Met Ala Asp Asp Asn Lys Leu
 225 230 235 240
 Phe Arg Glu Glu Phe Asn Ala Leu Pro Ala Cys Pro Ile Gln Ala Thr
 245 250 255
 Cys Glu Ala Ala Ser Lys Glu Glu Asn Lys Glu Lys Asn Arg Tyr Val
 260 265 270
 Asn Ile Leu Pro Tyr Asp His Ser Arg Val His Leu Thr Pro Val Glu
 275 280 285
 Gly Val Pro Asp Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asn Gly Tyr
 290 295 300
 Gln Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro Lys Glu Glu Thr
 305 310 315 320
 Val Asn Asp Phe Trp Arg Met Ile Trp Glu Gln Asn Thr Ala Thr Ile
 325 330 335
 Val Met Val Thr Asn Leu Lys Glu Arg Lys Glu Cys Lys Cys Ala Gln
 340 345 350
 Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Ser
 355 360 365
 Val Glu Asp Val Thr Val Leu Val Asp Tyr Thr Val Arg Lys Phe Cys
 370 375 380
 Ile Gln Gln Val Gly Asp Met Thr Asn Arg Lys Pro Gln Arg Leu Ile
 385 390 395 400
 Thr Gln Phe His Phe Thr Ser Trp Pro Asp Phe Gly Val Pro Phe Thr
 405 410 415
 Pro Ile Gly Met Leu Lys Phe Leu Lys Lys Val Lys Ala Cys Asn Pro

420	425	430
Gln Tyr Ala Gly Ala Ile Val Val His Cys Ser Ala Gly Val Gly Arg 435 440 445		
Thr Gly Thr Phe Val Val Ile Asp Ala Met Leu Asp Met Met His Thr 450 455 460		
Glu Arg Lys Val Asp Val Tyr Gly Phe Val Ser Arg Ile Arg Ala Gln 465 470 475 480		
Arg Cys Gln Met Val Gln Thr Asp Met Gln Tyr Val Phe Ile Tyr Gln 485 490 495		
Ala Leu Leu Glu His Tyr Leu Tyr Gly Asp Thr Glu Leu Glu Val Thr 500 505 510		
Ser Leu Glu Thr His Leu Gln Lys Ile Tyr Asn Lys Ile Pro Gly Thr 515 520 525		
Ser Asn Asn Gly Leu Glu Glu Glu Phe Lys Lys Leu Thr Ser Ile Lys 530 535 540		
Ile Gln Asn Asp Lys Met Arg Thr Gly Asn Leu Pro Ala Asn Met Lys 545 550 555 560		
Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn Arg Val Ile 565 570 575		
Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val Asn Ala Ser 580 585 590		
Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala Ser Gln Gly 595 600 605		
Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile Trp Glu Trp 610 615 620		
Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu Arg Gly Gln 625 630 635 640		
Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val Ser Tyr Gly 645 650 655		
Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu Ser Tyr Thr 660 665 670		
Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys Ser Arg Gln 675 680 685		
Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly Ile Pro Ser 690 695 700		
Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln Lys Gln Gln 705 710 715 720		
Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser Ala Gly Ala 725 730 735		
Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu Glu Arg Val 740 745 750		
Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys Ser Leu Arg 755 760 765		
Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr Glu Phe Cys 770 775 780		

Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn
785 790 795 800

Phe Lys

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGATTCTT	GGTTCATTCT	TGTTCTGCTC	GGCAGTGGTC	TGATATGTGT	CAGTGCCAAC	60
AATGCTACCA	CAGTTGCACC	TTCTGTAGGA	ATTACAAGAT	TAATTAAGTC	ATCAACGGCA	120
GAACCAAGTTA	AAGAAGAGGC	CAAACTTCA	AATCCAAGTT	CTTCACTAAC	TTCTCTTTCT	180
GTGGCACCAA	CATTACAGCC	AAATATAACT	CTGGGACCCA	CCTATTTAAC	CACTGTCAAT	240
TCTTCAGACT	CTGACAATGG	GACCACAAGA	ACAGCAAGCA	CCAATTCTAT	AGGCATTACA	300
ATTTACCAA	ATGGAACGTG	GCTTCAGAT	AACCAGTTCA	CGGATGCCAG	AACAGAACCC	360
TGGGAGGGGA	ATTCCAGCAC	CGCAGCAACC	ACTCCAGAAA	CTTCCCTCC	TTCAGGTAAT	420
TCTGACTCGA	AGGACAGAAG	AGATGAGACA	CCAATTATTG	CGGTGATGGT	GGCCCTGTCC	480
TCTCTGCTAG	TGATCGTGTT	TATTATCATA	GTTTTGTACA	TGTTAAGGTT	TAAGAAATAC	540
AAGCAAGCTG	GGAGCCATTC	CAATTCTTTC	CGCTTATCCA	ACGGCCGCAC	TGAGGATGTG	600
GAGCCCCAGA	GTGTGCCACT	TCTGGCCAGA	TCCCCAAGCA	CCAACAGGAA	ATACCCACCC	660
CTGCCCCGTG	ACAAGCTGGA	AGAGGAAATT	AACCGGAGAA	TGGCAGACGA	CAATAAGCTC	720
TTCAGGGAGG	AATTCAACGC	TCTCCCTGCA	TGTCCTATCC	AGGCCACCTG	TGAGGCTGCT	780
TCCAAGGAGG	AAAACAAGGA	AAAAAATCGA	TATGTAAACA	TCTTGCCCTTA	TGACCACTCT	840
AGAGTCCACC	TGACACCGGT	TGAAGGGGTT	CCAGATTCTG	ATTACATCAA	TGCTTCATTC	900
ATCAACGGTT	ACCAAGAAAA	GAACAAATTC	ATTGCTGCAC	AAGGACCAAA	AGAAGAAACG	960
GTGAATGATT	TCTGGCGGAT	GATCTGGGAA	CAAAACACAG	CCACCATCGT	CATGGTTACC	1020
AACCTGAAGG	AGAGAAAGGA	GTGCAAGTGC	GCCCAGTACT	GGCCAGACCA	AGGCTGCTGG	1080
ACCTATGGGA	ATATTCGGGT	GTCTGTAGAG	GATGTGACTG	TCCTGGTGGA	CTACACAGTA	1140
CGGAAGTTCT	GCATCCAGCA	GGTGGGCGAC	ATGACCAACA	GAAAGCCACA	GCGCCTCATC	1200
ACTCAGTTCC	ACTTTACCAG	CTGGCCAGAC	TTTGGGGTGC	CTTTTACCCC	GATCGGCATG	1260
CTCAAGTTCC	TCAAGAAGGT	GAAGGCCTGT	AACCCTCAGT	ATGCAGGGGC	CATCGTGGTC	1320
CACTGCAGTG	CAGGTGTAGG	GCGTACAGGT	ACCTTTGTCC	TCATTGATGC	CATGCTGGAC	1380
ATGATGCATA	CAGAACGGAA	GGTGGACGTG	TATGGCTTTG	TGAGCCGGAT	CCGGGCACAG	1440
CGCTGCCAGA	TGGTGCAAAC	CGATATGCAG	TATGTCTTCA	TATACCAAGC	CCTTCTGGAG	1500

CATTATCTCT ATGGAGATAC AGAACTGGAA GTGACCTCTC TAGAAACCCA CCTGCAGAAA	1560
ATTTACAACA AAATCCCAGG GACCAGCAAC AATGGATTAG AGGAGGAGTT TAAGAAGTTA	1620
ACATCAATCA AAATCCAGAA TGACAAGATG CGGACTGGAA ACCTTCCAGC CAACATGAAG	1680
AAGAACCGTG TTTTACAGAT CATTCCATAT GAATTCAACA GAGTGATCAT TCCAGTTAAG	1740
CGGGGCGAAG AGAATACAGA CTATGTGAAC GCATCCTTTA TTGATGGCTA CCGGCAGAAG	1800
GACTCCTATA TCGCCAGOCA GGGCCCTCTT CTCCACACAA TTGAGGACTT CTGGCGAATG	1860
ATCTGGGAGT GGAAATCCTG CTCTATCGTG ATGCTAACAG AACTGGAGGA GAGAGGCCAG	1920
GAGAAGTGTG CCCAGTACTG GCCATCTGAT GGACTGGTGT CCTATGGAGA TATTACAGTG	1980
GAACTGAAGA AGGAGGAGGA ATGTGAGAGC TACACCGTCC GAGACCTCCT GGTCACCAAC	2040
ACCAGGGAGA ATAAGAGCCG GCAGATCCGG CAGTTCCACT TCCATGGCTG GCCTGAAGTG	2100
GGCATCCCCA GTGACGGAAA GGGCATGATC AGCATCATCG CCGCCGTGCA GAAGCAGCAG	2160
CAGCAGTCAG GGAACCACCC CATCACCGTG CACTGCAGCG CCGGGGCAGG AAGGACGGGG	2220
ACCTTCTGTG CCCTGAGCAC CGTCCTGGAG CGTGTGAAAG CAGAGGGGAT TTTGGATGTC	2280
TTCCAGACTG TCAAGAGCCT GCGGCTACAG AGGCCACACA TGGTCCAGAC ACTGGAACAG	2340
TATGAGTTCT GCTACAAGGT GGTGCAGGAG TATATTGATG CATTCTCAGA TTATGCCAAC	2400
TTCAAGTAA	2409

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Asp	Ser	Trp	Phe	Ile	Leu	Val	Leu	Phe	Gly	Ser	Gly	Leu	Ile	His
1				5					10					15	
Val	Ser	Ala	Asn	Asn	Ala	Thr	Thr	Val	Ser	Pro	Ser	Leu	Gly	Thr	Thr
			20					25					30		
Arg	Leu	Ile	Lys	Thr	Ser	Thr	Thr	Glu	Leu	Ala	Lys	Glu	Glu	Asn	Lys
		35					40					45			
Thr	Ser	Asn	Ser	Thr	Ser	Ser	Val	Ile	Ser	Leu	Ser	Val	Ala	Pro	Thr
		50				55					60				
Phe	Ser	Pro	Asn	Leu	Thr	Leu	Glu	Pro	Thr	Tyr	Val	Thr	Thr	Val	Asn
	65				70				75						80
Ser	Ser	His	Ser	Asp	Asn	Gly	Thr	Arg	Arg	Ala	Ala	Ser	Thr	Glu	Ser
			85					90					95		
Gly	Gly	Thr	Thr	Ile	Ser	Pro	Asn	Gly	Ser	Trp	Leu	Ile	Glu	Asn	Gln
		100					105						110		
Phe	Thr	Asp	Ala	Ile	Thr	Glu	Pro	Trp	Glu	Gly	Asn	Ser	Ser	Thr	Ala
	115						120						125		

Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile
130 135 140

Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile
145 150 155 160

Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser
165 170 175

His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu
180 185 190

Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys
195 200 205

Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Glu Ile Asn Arg Arg
210 215 220

Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro
225 230 235 240

Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn
245 250 255

Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg
260 265 270

Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn
275 280 285

Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala
290 295 300

Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp
305 310 315 320

Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu Arg
325 330 335

Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Cys Trp Thr
340 345 350

Tyr Gly Asn Val Arg Val Ser Val Glu Asp Val Thr Val Leu Val Asp
355 360 365

Tyr Thr Val Arg Lys Phe Ser Ile Gln Gln Val Gly Asp Val Thr Asn
370 375 380

Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp Pro
385 390 395 400

Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu Lys
405 410 415

Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val His
420 425 430

Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp Ala
435 440 445

Met Leu Asp Met Met His Ser Glu Arg Lys Val Asp Val Tyr Gly Phe
450 455 460

Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp Met
465 470 475 480

Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu His Tyr Leu Tyr Gly

485										490					495				
Asp	Thr	Glu	Leu	Glu	Val	Thr	Ser	Leu	Glu	Thr	His	Leu	Gln	Lys	Ile				
			500						505				510						
Tyr	Asn	Lys	Ile	Pro	Gly	Thr	Ser	Asn	Asn	Gly	Leu	Glu	Glu	Glu	Phe				
		515					520					525							
Lys	Lys	Leu	Thr	Ser	Ile	Lys	Ile	Gln	Asn	Asp	Lys	Met	Arg	Thr	Gly				
		530				535					540								
Asn	Leu	Pro	Ala	Asn	Met	Lys	Lys	Asn	Arg	Val	Leu	Gln	Ile	Ile	Pro				
545					550					555					560				
Tyr	Glu	Phe	Asn	Arg	Val	Ile	Ile	Pro	Val	Lys	Arg	Gly	Glu	Glu	Asn				
				565					570					575					
Thr	Asp	Tyr	Val	Asn	Ala	Ser	Phe	Ile	Asp	Gly	Tyr	Arg	Gln	Lys	Asp				
			580					585					590						
Ser	Tyr	Ile	Ala	Ser	Gln	Gly	Pro	Leu	Leu	His	Thr	Ile	Glu	Asp	Phe				
		595					600					605							
Trp	Arg	Met	Ile	Trp	Glu	Trp	Lys	Ser	Cys	Ser	Ile	Val	Met	Leu	Thr				
		610				615					620								
Glu	Leu	Glu	Glu	Arg	Gly	Gln	Glu	Lys	Cys	Ala	Gln	Tyr	Trp	Pro	Ser				
625					630					635					640				
Asp	Gly	Leu	Val	Ser	Tyr	Gly	Asp	Ile	Thr	Val	Glu	Leu	Lys	Lys	Glu				
				645					650					655					
Glu	Glu	Cys	Glu	Ser	Tyr	Thr	Val	Arg	Asp	Leu	Leu	Val	Thr	Asn	Thr				
			660					665					670						
Arg	Glu	Asn	Lys	Ser	Arg	Gln	Ile	Arg	Gln	Phe	His	Phe	His	Gly	Trp				
		675				680						685							
Pro	Glu	Val	Gly	Ile	Pro	Ser	Asp	Gly	Lys	Gly	Met	Ile	Asn	Ile	Ile				
		690				695					700								
Ala	Ala	Val	Gln	Lys	Gln	Gln	Gln	Ser	Gly	Asn	His	Pro	Ile	Thr					
705					710				715					720					
Val	His	Cys	Ser	Ala	Gly	Ala	Gly	Arg	Thr	Gly	Thr	Phe	Cys	Ala	Leu				
				725				730					735						
Ser	Thr	Val	Leu	Glu	Arg	Val	Lys	Ala	Glu	Gly	Ile	Leu	Asp	Val	Phe				
			740					745					750						
Gln	Thr	Val	Lys	Ser	Leu	Arg	Leu	Gln	Arg	Pro	His	Met	Val	Gln	Thr				
			755				760					765							
Leu	Glu	Gln	Tyr	Glu	Phe	Cys	Tyr	Lys	Val	Val	Gln	Glu	Tyr	Ile	Asp				
		770				775					780								
Ala	Phe	Ser	Asp	Tyr	Ala	Asn	Phe	Lys											
785					790														

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCCGGC GAGTGAGGCG CTGACAGGGA CTCGCGGGGG CATCTTGAC AGACCCCTGG	60
ACCACGCCGC CATCGCAGCC TCCAGCCCAG TCCTCTCTCT GCGCTTCTC CTCGCCATGG	120
AGGCCGCCGA CCGCCGTCCG CGGGCTTCGA GCAGCGGACC GGGCCGGGCT GACCCCATGT	180
GGGCCGAGAG CCCGGTCCTG AGGCGGAGCT GCCGTGCGCG TCCCCGCGG TCCCGCCCCA	240
GCGCCGGGCT CGGTCAGCAT GGATTCCTGG TTCATTCTTG TCCTGTTTGG CAGTGGTCTA	300
ATACATGTTA GTGCCAACAA TGCTACTACA GTTTCACCTT CTTTAGGAAC GACAAGATTA	360
ATTAAACAT CAACAACAGA ATTGGCTAAG GAAGAGAATA AAACCTCAA TTCAACCTCT	420
TCAGTAATTT CTCTTTCTGT GGCACCAACA TTCAGCCCAA ACCTGACTCT GGAGCCCACC	480
TATGTGACTA CTGTTAATTC TTCACACTCT GACAATGGGA CCAGGAGGGC AGCCAGCAGC	540
GAATCTGGAG GCACTACCAT TTCCCCGAAC GGAAGCTGGC TTATTGAGAA CCAGTTCACG	600
GATGCCATAA CAGAACCCTG GGAGGGGAAC TCCAGCACTG CAGCAACCAC TCCAGAAACC	660
TTCCCCCGG CAGATGAGAC ACCAATTATT GCGGTGATGG TGGCCCTGTC CTCTCTGCTA	720
GTAATCGTGT TTATTATCAT AGTTCTGTAC ATGTTAAGGT TTAAGAAATA CAAGCAAGCT	780
GGGAGTCATT CCAACTCTTT CCGCCTGTCA AATGGCCGCA CGGAGGATGT GGAGCCCCAA	840
AGTGTACCAC TTCTGGCCAG GTCCCCGAGC ACCAACAGGA AGTACCCACC ACTGCCTGTG	900
GACAAGCTGG AAGAGGAGAT TAACCGGAGA ATGGCTGATG ACAATAAGCT CTTCAGAGAA	960
GAATTCAACG CTCTCCCTGC TTGTCCTATC CAGGCCACCT GTGAGGCTGC CTCCAAGGAA	1020
GAACAACAGG AAAAAAACCG CTATGTAAAC ATCCTGCCCT ATGACCACTC TAGAGTGCAC	1080
CTGACACCTG TTGAAGGGGT CCCAGATTCT GATTACATCA ACGCTTCATT CATTAAATGGC	1140
TACCAGGAAA AGAACAAAT CATCGCTGCA CAAGGACCAA AAGAAGAAAC AGTGAATGAC	1200
TTCTGGAGAA TGATATGGGA ACAAACACA GCTACTATTG TCATGGTGAC CAACCTGAAG	1260
GAGAGAAAGG AGTGTAATG TGCCAATAC TGGCCAGACC AAGGCTGCTG GACCTATGGG	1320
AATGTCCGTG TGTCTGTCTG GGATGTGACT GTTCTGGTGG ACTACACAGT ACGGAAATTC	1380
TCGATCCAGC AGGTGGGCGA CGTGACCAAC AGGAAACCAC AGCGCCTCAT CACTCAGTTC	1440
CACTTCACCA GCTGGCCAGA CTTTGGGGTG CTTTTCACCC CAATTGGCAT GCTCAAGTTC	1500
CTCAAGAAGG TGAAGGCCTG TAACCCTCAG TACGCAGGG CTATCGTGGT CCACTGCAGT	1560
GCAGGTGTAG GCGCACTGG CACCTTTGTT GTCATCGATG CCATGCTGGA CATGATGCAT	1620
TCGAGCGCA AAGTGGATGT ATATGGGTTT GTGAGCCGGA TCCGGGCCCCA GCGCTGCCAG	1680
ATGTTACAGA CAGACATGCA GTACGTCTTC ATATACCAGG CCCTTCTGGA GCATTATCTG	1740
TATGGGGACA CAGAACTGGA AGTGACTTCT CTAGAAACCC ACCTACAAA AATTTATAAC	1800
AAGATCCCAG GGAAGTAGCA CAACGGGTTA GAGGAGGAGT TTAAGAAATT AACTTCAATC	1860
AAAATCCAGA ATGACAAGAT GCGCACGGGA AACCTTCCAG CCAACATGAA GAAGAACCGG	1920

GTTTTACAGA TCATTCCATA TGAATTTAAC AGAGTGATCA TTCCAGTCAA ACGAGGCGAA	1980
GAGAACACAG ACTATGTGAA CGCATCCTTC ATTGATGGAT ACCGGCAGAA AGACTCCTAC	2040
ATTGCCAGCC AGGGCCCTCT TCTCCACACG ATTGAGGACT TCTGGCGAAT GATCTGGGAG	2100
TGGAAGTCCT GTTCTATCGT AATGCTGACA GAACTGGAAG AGAGAGGCCA GGAGAAGTGT	2160
GCCCAGTACT GGCCATCTGA TGGCCTGGTG TCCTACGGAG ACATCACAGT TGAGCTGAAG	2220
AAGGAGGAGG AATGTGAAAG CTACACTGTC CGAGACCTCC TGGTCACCAA CACCAGGGAG	2280
AACAAGAGTC GGCAAATCCG GCAGTTCCAC TTCCACGGCT GGCCTGAGGT GGGCATCCCC	2340
AGCGACGGCA AGGGCATGAT CAACATCATT GCAGCAGTGC AGAAGCAGCA GCAGCAGTCG	2400
GGGAACCATC CCATCACTGT GCACTGCAGT GCCGGGGCAG GACGGACAGG AACCTTCTGT	2460
GCCTTGAGCA CAGTCCTGGA ACGTGTGAAA GCAGAAGGAA TTTTAGATGT CTTCCAAACT	2520
GTCAAGAGCC TCGGGCTGCA GAGGCCACAC ATGGTCCAGA CACTGGAACA GTATGAATTC	2580
TGCTACAAGG TGGTACAGGA ATACATTGAC GCCTTTTCAG ATTATGCCAA CTTCAAGTGA	2640
CAGGTGACAA GGCCCACAGA CAGGAGAATT GCCTTTAATA TTTTGTAATA TTCTGTTTTT	2700
GTTAATATAC CCAAATTGT ATATATCTTA TAACTGTTTT AGAAATGGCA CATAGGCTTC	2760
TATTACCTGT TAGATGGAGA TTTTGTATGT AAATGTGTTA GCACTGATAG TCCTTTTCCA	2820
GTGTTTTATT GGGAATTAA TAGTGTGATA TTTGGGTGA TATAATGAAT TC	2872

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu	Pro	Tyr	Asp	Tyr	Asn
1			5						10					15	
Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala	Gly	Ser	Asn	Tyr	Ile
		20						25					30		
Asn	Ala	Ser	Tyr	Ile	Asp	Gly	Phe	Lys	Glu	Pro	Arg	Lys	Tyr	Ile	Ala
		35					40					45			
Ala	Gln	Gly	Pro	Arg	Asp	Glu	Thr	Val	Asp	Asp	Phe	Trp	Arg	Met	Ile
	50				55						60				
Trp	Glu	Gln	Lys	Ala	Thr	Val	Ile	Val	Met	Val	Thr	Arg	Cys	Glu	Glu
65				70					75					80	
Gly	Asn	Arg	Asn	Lys	Cys	Ala	Glu	Tyr	Trp	Pro	Ser	Met	Glu	Glu	Gly
			85						90					95	
Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile	Asn	Gln	His	Lys	Arg
		100						105					110		
Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile	Val	Asn	Lys	Lys	Glu

115	120	125
Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln Phe Thr Ser Trp Pro		
130	135	140
Asp His Gly Val Pro Glu Asp Pro His Leu Leu Leu Lys Leu Arg Arg		
145	150	155
Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly Pro Ile Val Val His		
165	170	175
Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Gly Ile Asp Ala		
180	185	190
Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp Val Tyr Gly Tyr		
195	200	205
Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val Gln Val Glu Ala		
210	215	220
Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu		
225	230	235

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 236 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser	
1	15
Arg Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile	
20	30
Asn Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala	
35	45
Ala Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile	
50	60
Trp Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu	
65	80
Arg Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Glu Trp	
85	95
Thr Tyr Gly Asn Ile Arg Val Ser Val Glu Asp Val Thr Val Leu Val	
100	110
Asp Tyr Thr Val Arg Lys Phe Cys Ile Gln Gln Val Gly Asp Met Thr	
115	125
Asn Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp	
130	140
Pro Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu	
145	155
Lys Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val	

	165		170		175
His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp					
	180		185		190
Ala Met Leu Asp Met Met His Thr Glu Arg Lys Val Asp Val Tyr Gly					
	195		200		205
Phe Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp					
	210		215		220
Met Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu					
	225		230		235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Lys His Lys Asn Arg Tyr Ile Asn Ile Val Ala Tyr Asp His Ser					
1	5		10		15
Arg Val Lys Leu Ala Gln Leu Ala Glu Lys Asp Gly Lys Leu Thr Asp					
	20		25		30
Tyr Ile Asn Ala Asn Tyr Val Asp Gly Tyr Asn Arg Pro Lys Ala Tyr					
	35		40		45
Ile Ala Ala Gln Gly Pro Leu Lys Ser Thr Ala Glu Asp Phe Trp Arg					
	50		55		60
Met Ile Trp Glu His Asn Val Glu Val Ile Val Met Ile Thr Asn Leu					
	65		70		75
Val Glu Lys Gly Arg Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly					
	85		90		95
Ser Glu Glu Tyr Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val					
	100		105		110
Leu Ala Tyr Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile					
	115		120		125
Lys Lys Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln					
	130		135		140
Tyr His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu					
	145		150		155
Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His Ala					
	165		170		175
Val Gly Pro Val Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly					
	180		185		190
Thr Tyr Ile Val Leu Asp Ser Met Leu Gln Gln Ile Gln His Glu Gly					
	195		200		205
Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg Ser Gln Arg Asn					

210	215	220
Tyr Leu Val Gln Thr Glu Glu Gln Tyr Val Phe Ile His Asp Thr Leu		
225	230	235 240
Val Glu		

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 245 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn	Lys	His	Lys	Asn	Arg	Tyr	Ile	Asn	Ile	Leu	Ala	Tyr	Asp	His	Ser
1				5					10					15	
Arg	Val	Lys	Leu	Arg	Pro	Leu	Pro	Gly	Lys	Asp	Ser	Lys	His	Ser	Asp
			20					25					30		
Tyr	Ile	Asn	Ala	Asn	Tyr	Val	Asp	Gly	Tyr	Asn	Lys	Ala	Lys	Ala	Tyr
		35					40					45			
Ile	Ala	Thr	Gln	Gly	Pro	Leu	Lys	Ser	Thr	Phe	Glu	Asp	Phe	Trp	Arg
	50					55					60				
Met	Ile	Trp	Glu	Gln	Asn	Thr	Gly	Ile	Ile	Val	Met	Ile	Thr	Asn	Leu
65					70					75					80
Val	Glu	Lys	Gly	Arg	Arg	Lys	Cys	Asp	Gln	Tyr	Trp	Pro	Thr	Glu	Asn
				85					90					95	
Ser	Glu	Glu	Tyr	Gly	Asn	Ile	Ile	Val	Thr	Leu	Lys	Ser	Thr	Lys	Ile
			100					105					110		
His	Ala	Cys	Tyr	Thr	Val	Arg	Arg	Phe	Ser	Ile	Arg	Asn	Thr	Lys	Val
		115					120					125			
Lys	Lys	Gly	Gln	Lys	Gly	Asn	Pro	Lys	Gly	Arg	Gln	Asn	Glu	Arg	Val
	130					135					140				
Val	Ile	Gln	Tyr	His	Tyr	Thr	Gln	Trp	Pro	Asp	Met	Gly	Val	Pro	Glu
145					150					155					160
Tyr	Ala	Leu	Pro	Val	Leu	Thr	Phe	Val	Arg	Arg	Ser	Ser	Ala	Ala	Arg
				165					170					175	
Met	Pro	Glu	Thr	Gly	Pro	Val	Leu	Val	His	Cys	Ser	Ala	Gly	Val	Gly
			180					185					190		
Arg	Thr	Gly	Thr	Tyr	Ile	Val	Ile	Asp	Ser	Met	Leu	Gln	Gln	Ile	Lys
		195					200					205			
Asp	Lys	Ser	Thr	Val	Asn	Val	Leu	Gly	Phe	Leu	Lys	His	Ile	Arg	Thr
	210					215					220				
Gln	Arg	Asn	Tyr	Leu	Val	Gln	Thr	Glu	Glu	Gln	Tyr	Ile	Phe	Ile	His
225					230					235					240
Asp Ala Leu Leu Glu															
245															

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: /label= Xaa
/note= "For the Consensus Sequence, Xaa = Lack of Consensus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Asn Lys His Lys Asn Arg Tyr Xaa Asn Ile Leu Xaa Tyr Asp His Ser
1           5           10           15
Arg Val Lys Leu Xaa Xaa Leu Xaa Xaa Lys Xaa Xaa Lys Xaa Ser Asp
20           25           30
Tyr Ile Asn Ala Xaa Tyr Xaa Asp Gly Tyr Asn Glu Pro Lys Xaa Tyr
35           40           45
Ile Ala Ala Gln Gly Pro Leu Lys Xaa Thr Val Glu Asp Phe Trp Arg
50           55           60
Met Ile Trp Glu Gln Asn Thr Xaa Val Ile Val Met Xaa Thr Asn Leu
65           70           75           80
Val Glu Lys Gly Arg Arg Lys Cys Xaa Gln Tyr Trp Pro Xaa Xaa Gly
85           90           95
Ser Glu Xaa Tyr Gly Asn Ile Xaa Val Thr Val Lys Xaa Val Xaa Val
100          105          110
Leu Ala Xaa Xaa Asp Tyr Thr Val Arg Lys Phe Xaa Xaa Arg Asn Thr
115          120          125
Lys Ile Xaa Lys Xaa Gly Xaa Lys Xaa Xaa Xaa Lys Gly Arg Xaa Xaa
130          135          140
Gly Arg Val Val Thr Gln Tyr His Xaa Thr Xaa Trp Pro Asp Met Gly
145          150          155          160
Val Pro Glu Tyr Pro Leu Pro Val Leu Xaa Phe Val Arg Xaa Val Xaa
165          170          175
Ala Ala Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa Val Val His Cys Ser Ala
180          185          190
Gly Val Gly Arg Thr Gly Thr Tyr Ile Val Ile Asp Xaa Met Leu Gln
195          200          205
Gln Ile Xaa Xaa Glu Xaa Xaa Val Xaa Val Tyr Gly Phe Xaa Lys His
210          215          220
Ile Arg Xaa Gln Arg Xaa Tyr Xaa Val Gln Thr Glu Glu Gln Tyr Xaa
225          230          235          240
Phe Ile His Xaa Ala Leu Xaa Glu
245

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Asn Lys Ser Lys Asn Arg Asn Ser Asn Val Ile Pro Tyr Asp Tyr Asn
1      5      10      15
Arg Val Pro Leu Lys His Glu Leu Glu Met Ser Lys Glu Ser Glu His
20      25      30
Asp Ser Asp Glu Ser Ser Asp Asp Asp Ser Asp Ser Glu Glu Pro Ser
35      40      45
Lys Tyr Ile Asn Ala Ser Phe Ile Met Ser Tyr Trp Lys Pro Glu Val
50      55      60
Met Ile Ala Ala Gln Gly Pro Leu Lys Glu Thr Ile Gly Asp Phe Trp
65      70      75      80
Gln Met Ile Phe Gln Arg Lys Val Lys Val Ile Val Met Leu Thr Glu
85      90      95
Leu Lys His Gly Asp Gln Glu Ile Cys Ala Gln Tyr Trp Gly Glu Gly
100     105
Lys Gln Thr Tyr Gly Asp Ile Glu Val Asp Leu Lys Asp Thr Asp Lys
115     120     125
Ser Ser Thr Tyr Thr Leu Arg Val Phe Glu Leu Arg His Ser Lys Arg
130     135     140
Lys Asp Ser Arg Thr Val Tyr Gln Tyr Gln Tyr Thr Asn Trp Ser Val
145     150     155     160
Glu Gln Leu Pro Ala Glu Pro Lys Glu Leu Ile Ser Met Ile Gln Val
165     170     175
Val Lys Gln Lys Leu Pro Gln Lys Asn Ser Ser Glu Gly Asn Lys His
180     185     190
His Lys Ser Thr Pro Leu Leu Ile His Cys Arg Asp Gly Ser Gln Gln
195     200     205
Thr Gly Ile Phe Cys Ala Leu Leu Asn Leu Leu Glu Ser Ala Glu Thr
210     215     220
Glu Glu Val Val Asp Ile Phe Gln Val Val Lys Ala Leu Arg Lys Ala
225     230     235     240
Arg Pro Gly Met Val Ser Thr Phe Glu Gln Tyr Gln Phe Leu Tyr Asp
245     250     255
Val Ile Ala Ser
260

```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Asn Met Lys Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn
1           5           10           15
Arg Val Ile Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val
20           25           30
Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala
35           40           45
Ser Gln Gly Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile
50           55           60
Trp Glu Trp Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu
65           70           75           80
Arg Gly Gln Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val
85           90           95
Ser Tyr Gly Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu
100          105          110
Ser Tyr Thr Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys
115          120          125
Ser Arg Gln Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly
130          135          140
Ile Pro Ser Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln
145          150          155          160
Lys Gln Gln Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser
165          170          175
Ala Gly Ala Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu
180          185          190
Glu Arg Val Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys
195          200          205
Ser Leu Ala Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr
210          215          220
Glu Phe Cys Tyr Lys Val Val Gln Glu
225          230

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn Arg Glu Lys Asn Arg Thr Ser Ser Ile Ile Pro Val Glu Arg Ser
 1 5 10 15
 Arg Val Gly Ile Ser Ser Leu Ser Gly Glu Gly Thr Asp Tyr Ile Asn
 20 25 30
 Ala Ser Tyr Ile Met Gly Tyr Tyr Gln Ser Asn Glu Phe Ile Ile Thr
 35 40 45
 Gln His Pro Leu Leu His Thr Ile Lys Asp Phe Trp Arg Met Ile Trp
 50 55 60
 Asp His Asn Ala Gln Leu Val Val Met Ile Pro Asp Gly Gln Asn Met
 65 70 75 80
 Ala Glu Asp Glu Phe Val Tyr Trp Pro Asn Lys Asp Glu Pro Ile Asn
 85 90 95
 Cys Glu Ser Phe Lys Val Thr Leu Met Ala Glu Glu His Lys Cys Leu
 100 105 110
 Ser Asn Glu Glu Lys Leu Ile Ile Gln Asp Phe Ile Leu Glu Ala Thr
 115 120 125
 Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys Trp
 130 135 140
 Pro Asn Pro Asp Ser Pro Ile Ser Lys Thr Phe Glu Leu Ile Ser Val
 145 150 155 160
 Ile Lys Glu Glu Ala Ala Asn Arg Asp Gly Pro Met Ile Val His Asp
 165 170 175
 Glu His Gly Gly Val Thr Ala Gly Thr Phe Cys Ala Leu Thr Thr Leu
 180 185 190
 Met His Gln Leu Glu Lys Glu Asn Ser Val Asp Val Tyr Gln Val Ala
 195 200 205
 Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Ala Asp Ile Glu Gln
 210 215 220
 Tyr Gln Phe Leu Tyr Lys Val Ile Leu Ser
 225 230

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Lys Glu Lys Asn Arg Asn Ser Ser Val Val Pro Ser Glu Arg Ala
 1 5 10 15
 Arg Val Gly Leu Ala Pro Leu Pro Gly Met Lys Gly Thr Asp Tyr Ile
 20 25 30
 Asn Ala Ser Tyr Ile Met Gly Tyr Tyr Arg Ser Asn Glu Phe Ile Ile
 35 40 45

Thr Gln His Pro Leu Pro His Thr Thr Lys Asp Phe Trp Arg Met Ile
 50 55 60
 Trp Asp His Asn Ala Gln Ile Ile Val M t Leu Pro Asp Asn Gln Ser
 65 70 75 80
 Leu Ala Glu Asp Glu Phe Val Tyr Trp Pro Ser Arg Glu Glu Ser Met
 85 90 95
 Asn Cys Glu Ala Phe Thr Val Thr Leu Ile Ser Lys Asp Arg Leu Cys
 100 105 110
 Leu Ser Asn Glu Glu Gln Ile Ile Ile His Asp Phe Ile Leu Glu Ala
 115 120 125
 Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys
 130 135 140
 Trp Pro Asn Pro Asp Ala Pro Ile Ser Ser Thr Phe Glu Leu Ile Asn
 145 150 155 160
 Val Ile Lys Glu Glu Ala Leu Thr Arg Asp Gly Pro Thr Ile Val His
 165 170 175
 Asp Glu Tyr Gly Ala Val Ser Ala Gly Met Leu Cys Ala Leu Thr Thr
 180 185 190
 Leu Ser Gln Gln Leu Glu Asn Glu Asn Ala Val Asp Val Phe Gln Val
 195 200 205
 Ala Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Thr Asp Ile Glu
 210 215 220
 Gln Tyr Gln Phe Ile Tyr Lys Ala Arg Leu Ser
 225 230 235

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: /label= Xaa
 /note= "For the Consensus Sequence, Xaa = Lack of Consensus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Lys Glu Lys Asn Arg Asn Ser Ser Xaa Ile Pro Tyr Glu Arg Asn
 1 5 10 15
 Arg Val Gly Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Glu Glu Gly Thr
 35 40 45
 Asp Tyr Ile Asn Ala Ser Xaa Ile Met Gly Tyr Tyr Gln Ser Asn Glu
 50 55 60

Phe Ile Xaa Thr Gln Xaa Pro Leu Leu His Thr Ile Lys Asp Phe Trp
 65 70 75 80
 Arg Met Ile Trp Asp His Xaa Asn Ala Gln Ile Val Met Leu Xaa Xaa
 85 90 95
 Xaa Gln Xaa Xaa Ala Glu Xaa Glu Xaa Xaa Gln Tyr Trp Pro Ser Xaa
 100 105 110
 Gly Xaa Xaa Xaa Tyr Gly Asp Xaa Xaa Val Xaa Leu Lys Xaa Xaa Xaa
 115 120 125
 Asn Cys Glu Ser Xaa Thr Val Thr Xaa Xaa Xaa Glu Xaa Arg Xaa Cys
 130 135 140
 Leu Ser Asn Glu Xaa Arg Xaa Ile Ile Gln Asp Phe Ile Leu Glu Ala
 145 150 155 160
 Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys
 165 170 175
 Trp Pro Asn Pro Asp Xaa Pro Ile Ser Xaa Thr Xaa Glu Leu Ile Ser
 180 185 190
 Val Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Lys Xaa Glu Glu Ala
 195 200 205
 Xaa Asn Arg Xaa Xaa Xaa Asp Gly Pro Xaa Ile Val His Xaa Glu Xaa
 210 215 220
 Gly Ala Val Xaa Xaa Gly Thr Phe Cys Ala Leu Thr Thr Leu Leu Glu
 225 230 235 240
 Gln Leu Glu Xaa Glu Asn Xaa Val Asp Val Phe Gln Val Xaa Lys Met
 245 250 255
 Xaa Asn Leu Met Arg Pro Gly Xaa Xaa Xaa Xaa Ile Glu Gln Tyr Gln
 260 265 270
 Phe Leu Tyr Lys Val Ile Leu Ser
 275 280